



PCT

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/009,030A

DATE: 02/11/2003
TIME: 14:33:45

Input Set : A:\Bml41018.app
Output Set: N:\CRF4\02112003\J009030A.raw

3 <110> APPLICANT: ARAND, MICHAEL
 4 ARCHELAS, ALAIN ROBERT
 5 BARATI, JACQUES
 6 FURSTOSS, ROLAND
 8 <120> TITLE OF INVENTION: EPOXIDE HYDROLASES OF ASPERGILLUS ORIGIN
 10 <130> FILE REFERENCE: bml-410.018
 12 <140> CURRENT APPLICATION NUMBER: 10/009,030A
 C--> 13 <141> CURRENT FILING DATE: 2002-12-20
 15 <150> PRIOR APPLICATION NUMBER: PCT/FR00/01217
 16 <151> PRIOR FILING DATE: 2000-05-05
 18 <150> PRIOR APPLICATION NUMBER: FR 99/05711
 19 <151> PRIOR FILING DATE: 1999-05-05
 21 <160> NUMBER OF SEQ ID NOS: 8
 23 <170> SOFTWARE: PatentIn Ver. 2.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1197
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Aspergillus niger
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (1)..(1194)
 34 <400> SEQUENCE: 1
 35 atg tcc gct ccg ttc gcc aag ttt ccc tcg tcg gcg agc att tcg cct 48
 36 Met Ser Ala Pro Phe Ala Lys Phe Pro Ser Ser Ala Ser Ile Ser Pro
 37 1 5 10 15
 39 aat cct ttc acg gtc tct atc ccg gat gaa cag ttg gat gac ttg aaa 96
 40 Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gln Leu Asp Asp Leu Lys
 41 20 25 30
 43 acc ctc gtc cga ctg tcc aag att gct cct ccc acc tat gag agc ctg 144
 44 Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu
 45 35 40 45
 47 caa gcg gat ggc cggtt ggc atc act tct gaa tgg ctg aca act atg 192
 48 Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
 49 50 55 60
 51 cgg gag aaa tgg ctc tcg gag ttt gac tgg cga cca ttt gaa gct cga 240
 52 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
 53 65 70 75 80
 55 ctg aac tct ttc cct cag ttt act aca gag atc gag ggt ctc acg att 288
 56 -Leu-Asn-Ser-Phe-Pro-Gln-Phe-Thr-Thr-Glu-Ile-Glu-Gly-Leu-Thr-Ile
 57 85 90 95
 59 cac ttt gct gct ctc ttc tcc gag agg gag gag gat gct gtg cct atc gca 336
 60 His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala
 61 100 105 110

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63 ttg ctc cat ggt tgg ccc ggc agc ttc gtt gag ttc tac cca atc ctg	384
64 Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu	
65 115 120 125	
67 cag cta ttc cg ^g gag tac acc cct gag act ctg cca ttc cat ctg	432
68 Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu	
69 130 135 140	
71 gtt gtt ccg tcc ctt cct ggg tat act ttt tca tct ggt ccc ccg ctg	480
72 Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu	
73 145 150 155 160	
75 gac aag gac ttc ggc ttg atg gac aac gcc ccg gtc gta gac cag ttg	528
76 Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu	
77 165 170 175	
79 atg aag gac ctc ggg ttc gga agt ggt tat att att cag gga ggt gat	576
80 Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp	
81 180 185 190	
83 att ggt agc ttt gtt gga cga ctg ttg ggc gtg ggt ttc gac gcc tgc	624
84 Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys	
85 195 200 205	
87 aaa gcg gtt cat ttg aac ctg tgc gca atg agg gct ccc cct gag ggc	672
88 Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly	
89 210 215 220	
91 ccg tca att gag agc ttg tcc gca gcg gag aag gag gga atc gcg cga	720
92 Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg	
93 225 230 235 240	
95 atg gag aag ttc atg acc gat ggc tta gct tat gcc atg gag cac agt	768
96 Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser	
97 245 250 255	
99 act cgg ccc agt act att ggc cac gtg ctg tcc agc agt ccg atc gca	816
100 Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala	
101 260 265 270	
103 tta ctt gca tgg att ggt gag aaa tat ctc caa tgg gtg gat aaa ccc	864
104 Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro	
105 275 280 285	
107 ctc cct tct gag acc atc ctc gag atg gtg agc ctg tat tgg ctg acg	912
108 Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr	
109 290 295 300	
111 gaa agt ttc ccg ccg gca att cat acc tac cgc gag act acc cca act	960
112 Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr	
113 305 310 315 320	
115 gcc tcc gct ccc aat gga gcg aca atg ctt cag aag gaa tta tat att	1008
116 Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile	
117 325 330 335	
119 cac aag ccg ttt ggg ttc tcc ttc ccc aag gac ctt tgt cct gtg	1056
120 His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val	
121 340 345 350	
123 cct ccg agc tgg att gct aca acg gga aat cta gta ttc ttc ccg gat	1104
124 Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp	
125 355 360 365	
127 cat gca gag gga cac ttt gcc gca ttg gag cgt cca cgc gag ctg	1152

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Output Set: N:\CRF4\02112003\J009030A.raw

128 His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu
129 370 375 380
131 aag acc gac ctg aca gca ttt gtc gag cag gtg tgg cag aag tag 1197
132 Lys Thr Asp Leu Thr Ala Phe Val Glu Gln Val Trp Gln Lys
133 385 390 395
136 <210> SEQ ID NO: 2
137 <211> LENGTH: 398
138 <212> TYPE: PRT
139 <213> ORGANISM: Aspergillus niger
141 <400> SEQUENCE: 2
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143 1 5 10 15
145 Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gln Leu Asp Asp Leu Lys
146 20 25 30
148 Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu
149 35 40 45
151 Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
152 50 55 60
154 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
155 65 70 75 80
157 Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile
158 85 90 95
160 His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala
161 100 105 110
163 Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu
164 115 120 125
166 Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu
167 130 135 140
169 Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu
170 145 150 155 160
172 Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu
173 165 170 175
175 Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp
176 180 185 190
178 Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys
179 195 200 205
181 Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly
182 210 215 220
184 Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg
185 225 230 235 240
187 Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser
188 245 250 255
190 Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala
191 260 265 270
193 Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro
194 275 280 285
196 Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr
197 290 295 300
199 Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr

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200	305	310	315	320
202	Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile			
203	325	330	335	
205	His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val			
206	340	345	350	
208	Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp			
209	355	360	365	
211	His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu			
212	370	375	380	
214	Lys Thr Asp Leu Thr Ala Phe Val Glu Gln Val Trp Gln Lys			
215	385	390	395	
218	<210> SEQ ID NO: 3			
219	<211> LENGTH: 21			
220	<212> TYPE: DNA			
221	<213> ORGANISM: Artificial Sequence			
223	<220> FEATURE:			
224	<223> OTHER INFORMATION: Description of Artificial Sequence: Primer			
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231	<211> LENGTH: 20			
232	<212> TYPE: DNA			
233	<213> ORGANISM: Artificial Sequence			
235	<220> FEATURE:			
236	<223> OTHER INFORMATION: Description of Artificial Sequence: Primer			
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239	cgcgggcaat ccacacctac		20	
242	<210> SEQ ID NO: 5			
243	<211> LENGTH: 35			
244	<212> TYPE: DNA			
245	<213> ORGANISM: Artificial Sequence			
247	<220> FEATURE:			
248	<223> OTHER INFORMATION: Description of Artificial Sequence: Primer			
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254	<210> SEQ ID NO: 6			
255	<211> LENGTH: 24			
256	<212> TYPE: DNA			
257	<213> ORGANISM: Artificial Sequence			
259	<220> FEATURE:			
260	<223> OTHER INFORMATION: Description of Artificial Sequence: Primer			
262	<400> SEQUENCE: 6			
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267	<211> LENGTH: 32			
268	<212> TYPE: DNA			
269	<213> ORGANISM: Artificial Sequence			
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272	<223> OTHER INFORMATION: Description of Artificial Sequence: Primer			

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274 <400> SEQUENCE: 7
275 gctgaattca catgtccgct ccgttcggcca ag 32
278 <210> SEQ ID NO: 8
279 <211> LENGTH: 44
280 <212> TYPE: DNA
281 <213> ORGANISM: Artificial Sequence
283 <220> FEATURE:
284 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
285 oligonucleotide
287 <400> SEQUENCE: 8
288 ccatggaaat tctcgagatc taagcttagt catcagctgc atgg 44

VERIFICATION SUMMARY
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Input Set : A:\Bml41018.app
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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date